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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 6, 2004, 19:35:16; Search time 12.1875 Seconds (without alignments) 39.474 Million cell updates/sec

US-10-618-644-1 26 1 YVVFK 5 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | actin depolymerizi | | Gy5 - | glycinin A3B4 (pla | 3B4 | glycinin A3B4 (pla | 3B4 | UDP-sugar hydrolas | glycinin A3B4 (pla | probable phloem-sp | legumin B (clone p | hypothetical prote | legumin B LegK pre | hypothetical prote | 0 | hypothetical prote | hypothetical prote | Вр | × | legumin B LegJ pre | glycinin G5 precur | ı m | ble legumir | mecRl protein - St | methicillin resist | mecRl protein - St | hypothetical prote | cell division cont | GP80 precursor - s |
|-----------------------|--------------------|--------|--------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| QI | G84717 | T43245 | PQ0200 | PQ0810 | PQ0806 | PQ0809 | PQ0807 | S04172 | PQ0808 | E84434 | S04321 . | T24143 | 500337 | T28978 | AC0234 | T47039 | G86170 | S44268 | S26688 | 800336 | FWSYG3 | S37241 | T06453 | BWSAM1 | T44117 | S20575 | T19692 | S15038 | T31344 |
| 08 | ~ | ~ | ~ | ~ | ~ | ~ | ~ | ч | ~ | ~ | ~ | ~ | ~ | ~ | ~ | ~ | ~ | ~ | 7 | ~ | ч | ~ | ~ | - | ~ | ~ | 7 | ~ | 7 |
| Query Match Length | 132 | 137 | 186 | 191 | 236 | 238 | 243 | 251 | 251 | 317 | 338 | 340 | 350 | 373 | 449 | 449 | 452 | 485 | 200 | 503 | 516 | 564 | 266 | 585 | 585 | 585 | 915 | 974 | 1289 |
| Query Match | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 |
| Score | 26 | 56 | 26 | 26 | 26 | 56 | 56 | 56 | 26 | 26 | 26 | 26 | 56 | 56 | 26 | 56 | 26 | 26 | 26 | 56 | 56 | 26 | 26 | 36 | 26 | 36 | 26 | 26 | 56 |
| Regult No. | - | 7 | 9 | 4 | ហ | 9 | 7 | 60 | 0 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 |

| fatty acid synthas hypothetical prote | hypothetical prote conserved hypothet | actin depolymerizi | hypothetical prote | small protein smpB | hypothetical prote | hypothetical prote | CDPdiacylglycerol | hypothetical prote | probable phloem-sp | glycinin A5A4B3 pr | hypothetical prote | probable phloem-sp | hypothetical prote |
|---------------------------------------|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A87058 T18122 | T17717 H70429 | B84543 | T17748 | B64106 | A71009 | F64860 | AF0942 | T41936 | G84434 | PQ0199 | F72259 | G84435 | T05522 |
| 0 0 | 00 | 1 (1 | ~ | ~ | 7 | 7 | ~ | ~ | 7 | ~ | 7 | ~ | 7 |
| 3076 | 98 | 132 | 158 | 161 | 176 | 194 | 251 | 258 | 265 | 268 | 270 | 272 | 281 |
| 100.0 | 96.2 | 96.2 | 96.2 | 96.2 | 96.2 | 96.2 | 96.2 | 96.2 | 96.2 | 96.2 | 96.2 | 96.2 | 96.2 |
| 26 | 25 | 25 | 52 | 52 | 25 | 25 | 52 | 52 | 25 | 25 | 25 | 25 | 25 |
| 30 | 3.5 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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G84717
G84717
G84717
G84717
G84717
G84717
G84717
G84717
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana
C.Species: Arabidopsis thaliana
C.Species: Arabidopsis thaliana, C.Y.;
R.Lin, X.; Kaul, S.-P. Roungley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Noffat, K.S.; Cronia, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Gruss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Mature 402, 761-768, 1999
A; Title: Sequence and analygis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <STO>
A;Cross-references: GB:AE002093; NID:g4432815; PIDN:AAD20665.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g31200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 2
C,Superfamily: cofilin
RESULT 1
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Gaps ö 100.0%; Score 26; DB 2; Length 132; 100.0%; Pred. No. 34; cive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 5; Conservative

ö

|||||| 22 YVVFK 26 1 YVVFK 5 ò

probable actin-depolymerizing factor - fission yeast (Schizosaccharomyces pombe) c; species: Schizosaccharomyces pombe C; species: Schizosaccharomyces pombe C; species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 C; Accession: T43245; T38120
R; Kawamukai, M. Submitted to the EMBL Data Library, December 1996 A; Description: S. pombe CDNA for actin depolymerizing factor. A; Reference number: 22236
A; Accession: T43245 A; Accession: T43245 A; Accession: T43245 A; Connor; R: Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. Bubmitted to the EMBL Data Library, August 1996 A; Residues: 1-137 < KAW A; Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. Bubmitted to the EMBL Data Library, August 1996 A; Accession: T38120 A; Accession: T38120 A; Accession: T38120 A; Molecule type: DNA

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Gramman A3B4 - soybean (cv. Mandarin) (fragment)
NiAlternate names: 11S globulin; basic and acidic chains
NiAlternate names: 11S globulin; basic and acidic chains
Cispeciaes: Glycine max (soybean)
C;Bate: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: PQ0806
C;Accession: PQ0806
C;Accession: Appl. Genet. 78, 852-856, 1989
A;Title: An attempt to elucidate the origin of cultivated soybean via comparison of nucl. A;Reference number: PQ0806
A;Reference number: PQ0806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycinin A3B4 (plasmid pSPGLI) - Glycine soja (strain L23) (fragment)
NyAlternate names: 11S globulin; basic and acidic chains
NyContains: glycinin B4 chain
NyContains: glycinin B4 chain
C;Species: Glycine soja
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
R;Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
Theor. Appl. Genet. 78, 852-856, 1999
A;Title: An attempt to elucidate the origin of cultivated soybean via comparison of nucl
A;Reference number: PQ0806
A;Accession: PQ0806
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N;Alternate names: 11S globulin; basic and acidic chains
C;Species: Glycine max (soybean)
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: PQ0807
R;Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-236 <ZAK>
A,Residues: 1-236 <ZAK>
C,COSS-Teferences: UNIPROT:P93708; UNIPROT:P93707; UNIPROT:Q39922
C,Superfamily: glycinin
C;Keywords: seed; storage protein
F;84-236/Froduct: glycinin, B4 chain #status predicted <GB4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 26; DB 2; Length 236; Best Local Similarity 100.0%; Pred. No. 59; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 100.0%; Score 26; DB 2; Length 238; Similarity 100.0%; Pred. No. 60; 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q7M210
C;Superfamily: glychin
C;Keywords: seed; storage protein
F:99-238/Product: glycinin B4 chain #status predicted <GLB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                    |||||
139 YVVFK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 YVVFK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-238 <ZAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 YVVFK 203
               1 YVVFK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YVVFK 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riscallon, B.; Thanh, V.H.; Floener, L.A.; Nielsen, N.C.
Theor. Appl. Genet. 70, 510-519, 1991
A; Title: Identification and characterization of DNA clones encoding group-II glycinin sy A; Reference number: PQ0199
A; Accession: PO0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jycinin A3B4 (plasmid pSPGD41) - Glycine soja (strain L582) (fragment)
NyAlternate names: 11S globulin; basic and acidic chains
NyContains: glycinin B4 chain
C;Species: Glycine soja
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: PQ0810
R;Zakharova, E.S.; Epishin, X, Vinetski, Y.P.
Theor. Appl. Genet. 78, 852-856, 1989
A;Title: An attempt to elucidate the origin of cultivated soybean via comparison of nucl
A;Reference number: PQ0806
A;Accession: PQ0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A/Cross-references: UNIPROT:P93708
A/Experimental source: embryo, strain CX635-1-1-1
A/Experimental source: embryo, strain CX635-1-1-1
A/NOTE: the authors translated the codon NAA for residue 93 as Gln and AGA for residue C/Superfamily: glycinin
C/Keywords: seed; storage protein
F;16-186/Product: glycinin B4 chain (fragment) #status predicted <MAT>
A;Cross-references: EMBL:Z98600; PIDN:CAB11258.1; GSPDB:GN00066; SPDB:SPAC20G4.06c
A;Experimental source: strain 972h-; cosmid c20G4
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C;Species: Glycine max (soybean)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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0
                                                                                                                                                                                                                                                                                              100.0%; Score 26; DB 2; Length 137; 100.0%; Pred. No. 35; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th Similarity 100.0%; Score 26; DB 2; Length 186; Similarity 100.0%; Pred. No. 47; 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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F;39-191/Product: glycinin B4 chain #status predicted <GB4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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A;Residues: 1-191 <ZAK>
A;Cross-references: UNIPROT:Q7M211
C;Superfamily: glycinin
                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                         A.Map position: 1
A.Introns: 1/3; 37/1
A.Note: adf1
C.Superfamily: cofilin
C.Keywords: actin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-186 <SCA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 5; Conserv
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                                                                                       A; Gene: SPAC20G4.06c
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T24143
hypothetical protein R10B8.1 - Caenorhabditis elegans
hypothetical caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24143
R;Ainscough, R
R;Ainscough, Caenorhabata Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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283 YVVFK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-317 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 YVVPK 189
                                                                                      199 YVVFK 203
                                        1 YVVFK 5
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R;Garrett, A.R.; Johnson, L.A.; Beacham, I.R.
Mol. Microbiol. 3, 177-186, 198
A;Tit.Le: Isolation, molecular characterization and expression of the ushB gene of Salmon A;Reference number: S04172; MUID:89343621; PMID:2548058
A;Accession: S04172
A;Molecule type: DNA
A;Residues: 1-251 cGAR>
A;Residues: 1-251 cGAR>
A;Coss-references: UNIPROT:P26219; EMBL:X13380; NID:947954; PIDN:CAA31757.1; PID:947955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
Theor. Appl. Genet. 78, 852-856, 1989
A;Title: An attempt to elucidate the origin of cultivated soybean via comparison of nucl genitor, Glycine soja.
A;Reference number: PQ0806
A;Reference number: PQ0806
                                             nucl
Theor. Appl. Genet. 78, 852-856, 1989
A.Title: An attempt to elucidate the origin of cultivated soybean via comparison of genitor, Glycine soja.
A.Reference number: PQ0806
A.Reference number: PQ0807
A.Molecule type: mRNA
A.Residues: 1-243 <ZAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: mRNA
A,Residues: 1-251 <ZAK>
A,Cross-references: UNIPROT:P93708; UNIPROT:P93707; UNIPROT:Q39922; UNIPROT:Q9SB12
C,Superfamily: glycinin
C,Keywords: seed; storage protein
F;99-251/Product: glycinin B4 chain #status predicted <GB4>
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N;Alternate names: 11S globulin; basic and acidic chains
N;Contains: glycinin B4 chain
C;Species: Glycine max (soybean)
C;Date: 110-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: PQ0808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UDP-sugar hydrolase precursor - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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C;Superfamily: glycinin
C;Keywords: seed; storage protein
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 251;
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C;Superfamily: CDP-diacylglycerol pyrophosphatase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-251/Product: UDP-sugar hydrolase #status predicted <MAT>
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Best Local Similarity 100...
S; Conservative
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Best Local Similarity
Matches 5; Conserv
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199 YVVFK 203
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Cjaccesion: E84434
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thalians.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:Q9ZVR6; GB:AE002093; NID:G3894158; PIDN:AAC78508.1; GSPDB:G
C;Genetics:
A;Gene: At2g02230
A;Map position: 2
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A;Residues: 1-338 <DOM>
A;Cross-references: UNIPROT:P14594; EMBL:M16890; NID:g169120; PIDN:AAA33678.1; PID:g169
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R;Domoney, C.; Barker, D.; Casey, R.
Bjant Mol. Biol. 7, 467-474, 1986
A;Title: The complete deduced amino acid sequences of legumin beta-polypeptides A;Reference number: $02306
A;Accession: $04321
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C;Species: Pisum sativum (garden pea)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
probable phloem-specific lectin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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F:1-161/Product: legumin B alpha chain (fragment) #status predicted
F:162-338/Product: legumin B beta chain #status predicted <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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100.0%; Pred. No. 79;
ive 0; Mismatches 0; Indels
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84;
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100.0%; Score 26;
Best Local Similarity 100.0%; Pred. No. 8
Matches 5; Conservative 0; Mismatche
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A;Gene: YPO1919
C;Superfamily: uncharacterized conserved protein
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                     A; Reference number: Z20550
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Matches 5; Conserv
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                             A;Accession: T24143
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Reaidues: 1-340 - WILL>
A;Reaidues: 1-340 - WILL>
A;Cxoss-references: UNIPROT:O17998; EMBL:Z81576; PIDN:CAB04643.1; GSPDB:GN00023; CESP:R1
A;Experimental source: clone R10E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            legumin B LegK precursor - garden pea (fragment)
N;Alternate names: minor legumin legK
C;Species: Pisum sativum (garden pea)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00337; S02306
R;Gatehouse, J.A.; Bown, D; Gilroy, J.; Levasseur, M.; Castleton, J.; Ellis, T.H.N.
Biochem. J. 250, 15-24, 1988
A;Title: Two genes encoding 'minor' legumin polypeptides in pea (Pisum sativum L.). Char A;Accession: S00336; MUID:88183306; PMID:3355508
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A; Residues: 132-350 < DOM>
A; Residues: 132-350 < DOM>
A; Cross-references: EMBL:M16903
A; Note: the nucleotide sequence contains a frameshift in codon 131
A; Note: translation of nucleotide sequence for residues 132-169 is not given
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A;Introns: 33/3; 225/3
C;Superfamily: glycinin
F;1-169/Product: legumin B alpha chain (fragment) #status experimental <ACH>F;170-350/Product: legumin B beta chain #status experimental <ACH>F;170-350/Product: legumin B beta chain #status experimental <BCH>F;170-350/Product: legumin B beta chain #status experimental <BCH>F;170-350/Product experimental <BCH>F;1
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Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cibacession: T28978
RiRohlfing, T.
submitted to the EMBL Data Library, January 1997
Aibescription: The sequence of C. elegans cosmid T28A11.
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Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels
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100.0%; Score 26; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: CESP:R10E8.1
A;Map position: 5
A;Introns: 13/2; 34/2; 253/3; 331/3
A; Reference number: Z19844
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291 YVVFK 295
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A.Accession: T28978
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Stoleus: 1-373 <ROH>
A.ROH>
A.ROH>
A.ROS-references: UNIPROT: P91509; EMBL: U80027; PIDN: AAC48124.1; GSPDB: GN00023; CESP:T2.A.Experimental source: strain Bristol N2; clone T28A11
A.Experimental source: strain Bristol N2; clone T28A11
A.Gene: CESP:T28A11.14
A.Gene: CESP:T28A11.14
A.Map position: 5
A.Introns: 52/3
C.Superfamily: Caenorhabditis transposon Tc1 hypothetical 32K protein
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C;Species: Yersinia pestis
C;Date: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 24-Nov-2003
C;Accession: AC0234
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B |
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A'Molecule type: DNA
A'Residues: 1-449 <KUR>
A'Cross-references: GB:AL590842; PIDN:CAC90735.1; PID:g15979938; GSPDB:GN00175
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